Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (*Cancelled*)

2. (*Previously presented*) The method of claim 85, wherein the excess amount of the first competitor peptide is about or more than 100-fold molar excess.

3. (*Cancelled*)

4. (*Currently amended*) The method of claim 85, wherein ~~said liquid phase condition includes~~ the incubating ~~the sample~~ is performed for about 2 to 20 hours.

5. (*Currently amended*) The method of claim 4, wherein ~~said liquid phase condition further includes~~ the incubating ~~the sample~~ is performed at about 21 °C.

6. (*Previously presented*) The method of claim 85, wherein the detectable label is a fluorophore.

7. (*Withdrawn*) The method of claim 6, wherein the monomer is attached to a solid support prior to determining the signal produced solely by the monomers in the sample.

8. (*Withdrawn*) The method of claim 7, wherein the MHC monomer or modified MHC monomer is biotinylated and the monomer is attached to the solid support via a biotin/avidin or streptavidin linkage.

9. (*Original*) The method of claim 6, wherein the fluorophore is fluorescein (FITC).

10-12. (*Cancelled*)

13. (*Currently amended*) The method of claim 85, wherein the HLA-A2 monomer is HLA-A*020~~Mart-1 26-35~~.

14. (*Original*) The method of claim 13, wherein the tracer peptide is HBc 18-27.

15. (*Cancelled*)

16. (*Withdrawn- previously presented*) The method of claim 85, wherein the method is repeated, except that a different competitor peptide is used.

17 - 19. (*Cancelled*)

20. (*Previously presented*) The method of claim 85, wherein the first competitor peptide comprises from about 8 to about 12 amino acids.

21. (*Currently amended*) The method of claim 20, wherein the HLA-A2 monomer or modified HLA-A2 monomer remains folded during the assay.

22. (*Currently amended*) The method of claim 20, wherein the tracer peptide comprises from about 8 to about 12 amino acids and peptide exchange occurs without unfolding or denaturing of the HLA-A2 monomer or modified HLA-A2 monomer.

23. (*Withdrawn- previously presented*) The method of claim 85, wherein the affinity of an exchanged competitor peptide is substantially equal to affinity of the first competitor peptide when folded into the binding pocket of the monomer during reconstitution of a ternary complex comprising the first competitor peptide and the monomer.

24. (*Withdrawn- previously presented*) The method of claim 85, wherein the modified MHC monomer comprises cell surface domains of the MHC monomer but does not comprise other domains of the MHC monomer.

25. (*Currently amended*) The method of claim 85, wherein the allele of the HLA-A2 monomer or modified HLA-A2 monomer is known and the ~~determining~~ quantifying

indicates whether the first competitor peptide is specific for the allele of the HLA-A2 monomer or modified HLA-A2 monomer.

26-78. (*Cancelled*)

79. (*Currently amended*) The method of claim ~~85~~ 88, wherein said expression system is a prokaryotic system.

80. (*Previously presented*) The method of claim 79, wherein said prokaryotic system is in *E. coli*.

81-84. (*Cancelled*)

85. (*Currently amended*) A method for ~~identifying~~ quantifying the exchange of ~~an~~ homogeneous template MHC-binding peptide ~~for an MHC monomer or modified MHC monomer~~ with a first competitor peptide on an MHC complex, said method comprising:

a) incubating in a first reaction vessel under a liquid phase condition:

(i) a ternary complex comprising:

at least one HLA-A2 monomer or at least one modified HLA-A2 monomer, ~~a~~ the homogeneous template MHC-binding peptide, and beta-2 microglobulin, ~~or~~

~~at least one modified HLA-A2 monomer, a template MHC-binding peptide, and beta-2 microglobulin,~~

wherein the HLA-A2 monomer or modified HLA-A2 monomer maintains the ability to assemble into a ternary complex with the template MHC-binding peptide and beta-2 microglobulin~~, and wherein said HLA-A2 monomer or modified HLA-A2 monomer is produced in an expression system selected from the group consisting of a prokaryotic system, a yeast system, a plant system, and an insect system~~;

(ii) an excess amount of a first competitor peptide; and

(iii) a tracer MHC-binding peptide tagged with a detectable label,

wherein ~~said~~ the tracer MHC-binding peptide competes with the first competitor peptide and the template peptide for binding to the monomer, and wherein the template MHC-binding peptide has a lower affinity than the tracer MHC-binding peptide for the monomer; ~~and~~

b) incubating in a second reaction vessel, run parallel to the first reaction vessel, under liquid phase condition:

(i) the ternary complex; and

(ii) the tracer MHC-binding peptide tagged with a detectable label,

wherein the tracer MHC-binding peptide displaces at least 90% of the template MHC-binding peptide; and

c) ~~determining~~ measuring a ~~difference in~~ signal produced by: ~~the detectable label in the sample as compared with signal produced solely by monomer obtained from the sample after the incubation, wherein the difference indicates the first competitor peptide is an MHC-binding peptide for the monomer.~~

(i) an MHC complex formed between the HLA-A2 monomer or modified HLA-A2 monomer, the tracer MHC-binding peptide, and beta-2 microglobulin in the presence of the first competitor peptide; and

(ii) an MHC complex formed between the HLA-A2 monomer or modified HLA-A2 monomer, the tracer MHC-binding peptide, and beta-2 microglobulin in the absence of the first competitor peptide; and

d) correlating the signals to quantify the exchange of the homogeneous template MHC-binding peptide with the first competitor peptide on the MHC complex.

86-87. (*Cancelled*)

88. (new) The method of claim 85, wherein the template MHC-binding peptide is Mart-1 26-35.

89. (*New*) The method of claim 85, wherein the HLA-A2 monomer or modified HLA-A2 monomer is produced in an expression system selected from the group consisting of a prokaryotic system, a yeast system, a plant system, and an insect system.

90. (*New*) The method of claim 85, wherein the quantifying involves determining the concentration of an MHC complex formed between the HLA-A2 monomer or modified HLA-A2 monomer, the first competitor peptide, and beta-2 microglobulin in a).

91. (*New*) The method of claim 85, wherein the quantifying involves determining the yield of an MHC complex formed between the HLA-A2 monomer or modified HLA-A2 monomer, the first competitor peptide, and beta-2 microglobulin in a).

92. (*New*) The method of claim 90, wherein concentration of the MHC complex is calculated from a standard curve.

93. (*New*) The method of claim 92, wherein the standard curve is obtained by incubating different concentrations of the ternary complex with the tracer MHC-binding peptide in the absence of the competitor peptide, and determining the signal produced by the MHC complex formed between the HLA-A2 monomer or modified HLA-A2 monomer, the tracer MHC-binding peptide, and beta-2 microglobulin at each concentration of the ternary complex.